



ENTERED PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/031,455

DATE: 07/17/2002

TIME: 09:41:06

Input Set : A:\2577-135US.ST25.txt

Output Set: N:\CRF3\07172002\J031455.raw

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3 <110> APPLICANT: Sundaresan, Venkatesan
4   Tantikanjana, Titima
6 <120> TITLE OF INVENTION: Gene Controlling Shoot Branching in Plants
8 <130> FILE REFERENCE: 2577-135
10 <140> CURRENT APPLICATION NUMBER: US 10/031,455
11 <141> CURRENT FILING DATE: 2002-01-22
13 <150> PRIOR APPLICATION NUMBER: PCT/SG00/00075
14 <151> PRIOR FILING DATE: 2000-05-23
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1614
22 <212> TYPE: DNA
23 <213> ORGANISM: Arabidopsis thaliana
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1611)
28 <223> OTHER INFORMATION:
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33 Met Ser Phe Thr Thr Ser Leu Pro Tyr Pro Phe His Ile Leu Leu Val
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36 ttt atc ctc tcc atg gca tca atc act cta ctg ggt cga ata ctc tca      96
37 Phe Ile Leu Ser Met Ala Ser Ile Thr Leu Leu Gly Arg Ile Leu Ser
38           20           25           30
40 agg ccc acc aaa acc aaa gac cga tct tgc cag ctt cct cct ggc cca      144
41 Arg Pro Thr Lys Thr Lys Asp Arg Ser Cys Gln Leu Pro Pro Gly Pro
42           35           40           45
44 cca gga tgg ccc atc ctc ggc aat cta ccc gaa cta ttc atg act cgt      192
45 Pro Gly Trp Pro Ile Leu Gly Asn Leu Pro Glu Leu Phe Met Thr Arg
46           50           55           60
48 cct agg tcc aaa tat ttc cgc ctt gcc atg aaa gag cta aaa aca gat      240
49 Pro Arg Ser Lys Tyr Phe Arg Leu Ala Met Lys Glu Leu Lys Thr Asp
50 65           70           75           80
52 ata gca tgt ttc aac ttt gcc ggc atc cgt gcc atc acc ata aac tcc      288
53 Ile Ala Cys Phe Asn Phe Ala Gly Ile Arg Ala Ile Thr Ile Asn Ser
54           85           90           95
56 gac gag agc gct aga gaa gcg ttt aga gag cga gac gca gat ttg gca      336
57 Asp Glu Ser Ala Arg Glu Ala Phe Arg Glu Arg Asp Ala Asp Leu Ala
58           100          105          110
60 gac cgg cct caa ctt ttc atc atg gag aca atc gga gac aat tac aaa      384
61 Asp Arg Pro Gln Leu Phe Ile Met Glu Thr Ile Gly Asp Asn Tyr Lys
62           115          120          125

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64 tca atg gga att tca ccg tac ggt gaa caa ttc atg aag atg aaa aga      432
65 Ser Met Gly Ile Ser Pro Tyr Gly Glu Gln Phe Met Lys Met Lys Arg
66      130      135      140
68 gtg atc aca acg gaa att atg tcc gtt aag acg ttg aaa atg ttg gag      480
69 Val Ile Thr Thr Glu Ile Met Ser Val Lys Thr Leu Lys Met Leu Glu
70 145      150      155      160
72 gct gca aga acc atc gaa gcg gat aat ctc ata gct tac gtt cac tcc      528
73 Ala Ala Arg Thr Ile Glu Ala Asp Asn Leu Ile Ala Tyr Val His Ser
74      165      170      175
76 atg tat caa cgg tcc gag acg gtc gat gtt aga gag ctc tcg agg gtt      576
77 Met Tyr Gln Arg Ser Glu Thr Val Asp Val Arg Glu Leu Ser Arg Val
78      180      185      190
80 tat ggt tac gca gtg acc atg cga atg ttg ttt gga agg aga cat gtt      624
81 Tyr Gly Tyr Ala Val Thr Met Arg Met Leu Phe Gly Arg Arg His Val
82      195      200      205
84 acg aaa gaa aac gtg ttt tct gat gat gga aga cta gga aac gcc gaa      672
85 Thr Lys Glu Asn Val Phe Ser Asp Asp Gly Arg Leu Gly Asn Ala Glu
86      210      215      220
88 aaa cat cat ctt gag gtg att ttc aac act ctt aac tgt tta ccg agt      720
89 Lys His His Leu Glu Val Ile Phe Asn Thr Leu Asn Cys Leu Pro Ser
90 225      230      235      240
92 ttt agt cca gcg gat tac gtg gaa cga tgg ttg aga ggt tgg aat gtt      768
93 Phe Ser Pro Ala Asp Tyr Val Glu Arg Trp Leu Arg Gly Trp Asn Val
94      245      250      255
96 gat ggt caa gag aag agg gtg aca gag aac tgt aac att gtt cgt agt      816
97 Asp Gly Gln Glu Lys Arg Val Thr Glu Asn Cys Asn Ile Val Arg Ser
98      260      265      270
100 tac aac aat ccc ata atc gac gag agg gtc cag ttg tgg agg gaa gaa      864
101 Tyr Asn Asn Pro Ile Ile Asp Glu Arg Val Gln Leu Trp Arg Glu Glu
102      275      280      285
104 ggt ggt aag gct gct gtt gaa gat tgg ctt gat acg ttc att acc cta      912
105 Gly Gly Lys Ala Ala Val Glu Asp Trp Leu Asp Thr Phe Ile Thr Leu
106      290      295      300
108 aaa gat caa aac gga aag tac ttg gtc aca cca gac gaa atc aaa gct      960
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110 305      310      315      320
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113 Gln Cys Val Glu Phe Cys Ile Ala Ala Ile Asp Asn Pro Ala Asn Asn
114      325      330      335
116 atg gag tgg aca ctt ggg gaa atg tta aag aac ccg gag att ctt aga      1056
117 Met Glu Trp Thr Leu Gly Glu Met Leu Lys Asn Pro Glu Ile Leu Arg
118      340      345      350
120 aaa gct ctg aag gag ttg gat gaa gta gtt gga aga gac agg ctt gtg      1104
121 Lys Ala Leu Lys Glu Leu Asp Glu Val Val Gly Arg Asp Arg Leu Val
122      355      360      365
124 caa gaa tca gac ata cca aat cta aac tac tta aaa gct tgt tgt aga      1152
125 Gln Glu Ser Asp Ile Pro Asn Leu Asn Tyr Leu Lys Ala Cys Cys Arg
126      370      375      380
128 gaa aca ttc aga att cac cca agt gct cat tat gtc cct tcc cat ctt      1200

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129 Glu Thr Phe Arg Ile His Pro Ser Ala His Tyr Val Pro Ser His Leu
130 385                      390                      395                      400
132 gcg cgt caa gat acc acc ctt ggg ggt tat ttc att ccc aaa ggt agc      1248
133 Ala Arg Gln Asp Thr Thr Leu Gly Gly Tyr Phe Ile Pro Lys Gly Ser
134                      405                      410                      415
136 cac att cat gta tgc cgc cct gga cta ggt cgt aac cct aaa ata tgg      1296
137 His Ile His Val Cys Arg Pro Gly Leu Gly Arg Asn Pro Lys Ile Trp
138                      420                      425                      430
140 aaa gat cca ttg gta tac aaa ccg gag cgt cac ctc caa gga gac gga      1344
141 Lys Asp Pro Leu Val Tyr Lys Pro Glu Arg His Leu Gln Gly Asp Gly
142                      435                      440                      445
144 atc aca aaa gag gtt act ctg gtg gaa aca gag atg cgt ttt gtc tcg      1392
145 Ile Thr Lys Glu Val Thr Leu Val Glu Thr Glu Met Arg Phe Val Ser
146                      450                      455                      460
148 ttt agc acc ggt cga cgt ggc tgc atc ggt gtt aaa gtc ggg acg atc      1440
149 Phe Ser Thr Gly Arg Arg Gly Cys Ile Gly Val Lys Val Gly Thr Ile
150 465                      470                      475                      480
152 atg atg gtt atg ttg ttg gct agg ttt ctt caa ggg ttt aac tgg aaa      1488
153 Met Met Val Met Leu Leu Ala Arg Phe Leu Gln Gly Phe Asn Trp Lys
154                      485                      490                      495
156 ctc cat caa gat ttt gga ccg tta agc ctc gag gaa gat gat gca tca      1536
157 Leu His Gln Asp Phe Gly Pro Leu Ser Leu Glu Glu Asp Asp Ala Ser
158                      500                      505                      510
160 ttg ctt atg gct aaa cct ctt cac ttg tcc gtt gag cca cgc ttg gca      1584
161 Leu Leu Met Ala Lys Pro Leu His Leu Ser Val Glu Pro Arg Leu Ala
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165 Pro Asn Leu Tyr Pro Lys Phe Arg Pro
166                      530                      535
169 <210> SEQ ID NO: 2
170 <211> LENGTH: 537
171 <212> TYPE: PRT
172 <213> ORGANISM: Arabidopsis thaliana
174 <400> SEQUENCE: 2
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177 1                      5                      10                      15
180 Phe Ile Leu Ser Met Ala Ser Ile Thr Leu Leu Gly Arg Ile Leu Ser
181                      20                      25                      30
184 Arg Pro Thr Lys Thr Lys Asp Arg Ser Cys Gln Leu Pro Pro Gly Pro
185                      35                      40                      45
188 Pro Gly Trp Pro Ile Leu Gly Asn Leu Pro Glu Leu Phe Met Thr Arg
189                      50                      55                      60
192 Pro Arg Ser Lys Tyr Phe Arg Leu Ala Met Lys Glu Leu Lys Thr Asp
193 65                      70                      75                      80
196 Ile Ala Cys Phe Asn Phe Ala Gly Ile Arg Ala Ile Thr Ile Asn Ser
197                      85                      90                      95
200 Asp Glu Ser Ala Arg Glu Ala Phe Arg Glu Arg Asp Ala Asp Leu Ala
201                      100                     105                     110
204 Asp Arg Pro Gln Leu Phe Ile Met Glu Thr Ile Gly Asp Asn Tyr Lys

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205          115          120          125
208 Ser Met Gly Ile Ser Pro Tyr Gly Glu Gln Phe Met Lys Met Lys Arg
209          130          135          140
212 Val Ile Thr Thr Glu Ile Met Ser Val Lys Thr Leu Lys Met Leu Glu
213 145          150          155          160
216 Ala Ala Arg Thr Ile Glu Ala Asp Asn Leu Ile Ala Tyr Val His Ser
217          165          170          175
220 Met Tyr Gln Arg Ser Glu Thr Val Asp Val Arg Glu Leu Ser Arg Val
221          180          185          190
224 Tyr Gly Tyr Ala Val Thr Met Arg Met Leu Phe Gly Arg Arg His Val
225          195          200          205
228 Thr Lys Glu Asn Val Phe Ser Asp Asp Gly Arg Leu Gly Asn Ala Glu
229          210          215          220
232 Lys His His Leu Glu Val Ile Phe Asn Thr Leu Asn Cys Leu Pro Ser
233 225          230          235          240
236 Phe Ser Pro Ala Asp Tyr Val Glu Arg Trp Leu Arg Gly Trp Asn Val
237          245          250          255
240 Asp Gly Gln Glu Lys Arg Val Thr Glu Asn Cys Asn Ile Val Arg Ser
241          260          265          270
244 Tyr Asn Asn Pro Ile Ile Asp Glu Arg Val Gln Leu Trp Arg Glu Glu
245          275          280          285
248 Gly Gly Lys Ala Ala Val Glu Asp Trp Leu Asp Thr Phe Ile Thr Leu
249          290          295          300
252 Lys Asp Gln Asn Gly Lys Tyr Leu Val Thr Pro Asp Glu Ile Lys Ala
253 305          310          315          320
256 Gln Cys Val Glu Phe Cys Ile Ala Ala Ile Asp Asn Pro Ala Asn Asn
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260 Met Glu Trp Thr Leu Gly Glu Met Leu Lys Asn Pro Glu Ile Leu Arg
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264 Lys Ala Leu Lys Glu Leu Asp Glu Val Val Gly Arg Asp Arg Leu Val
265          355          360          365
268 Gln Glu Ser Asp Ile Pro Asn Leu Asn Tyr Leu Lys Ala Cys Cys Arg
269          370          375          380
272 Glu Thr Phe Arg Ile His Pro Ser Ala His Tyr Val Pro Ser His Leu
273 385          390          395          400
276 Ala Arg Gln Asp Thr Thr Leu Gly Gly Tyr Phe Ile Pro Lys Gly Ser
277          405          410          415
280 His Ile His Val Cys Arg Pro Gly Leu Gly Arg Asn Pro Lys Ile Trp
281          420          425          430
284 Lys Asp Pro Leu Val Tyr Lys Pro Glu Arg His Leu Gln Gly Asp Gly
285          435          440          445
288 Ile Thr Lys Glu Val Thr Leu Val Glu Thr Glu Met Arg Phe Val Ser
289          450          455          460
292 Phe Ser Thr Gly Arg Arg Gly Cys Ile Gly Val Lys Val Gly Thr Ile
293 465          470          475          480
296 Met Met Val Met Leu Leu Ala Arg Phe Leu Gln Gly Phe Asn Trp Lys
297          485          490          495
300 Leu His Gln Asp Phe Gly Pro Leu Ser Leu Glu Glu Asp Asp Ala Ser
301          500          505          510

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308 Pro Asn Leu Tyr Pro Lys Phe Arg Pro
309 530 535

VERIFICATION SUMMARY

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